



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Jofuku, K. Diane
Okamuro, Jack K.
- (ii) TITLE OF INVENTION: Methods for Improving Seeds
- (iii) NUMBER OF SEQUENCES: 111
- (iv) CORRESPONDENCE ADDRESS:
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(C) CITY: San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94111-3834
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- C (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/879,827
(B) FILING DATE: 20-JUN-1997
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/700,152
(B) FILING DATE: 20-AUG-1996
- (viii) ATTORNEY/AGENT INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Tyr Arg Gly
1

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ala or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Arg or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Trp Glu Xaa Xaa
1

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1680 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1680
- (D) OTHER INFORMATION: /note= "Arabidopsis APETALA2 (AP2)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCTCTCTCT CTCTTTAGCT CTTTTTTTTT TTTTGTTC ATTAAGTTT TTATTTTATT	60
TTCTACCAAC CAAAAGCTTT TCTCTTTGGT TTCTCTTATT TAGCTTCTAA CCTTGAGGAG	120
AATATACCAG AGGATTGAAG TTTGAACCTT CAAAGATCAA AATCAAGAAA CCAAAAAAAAA	180
ACAAAAAAAA TGTGGGATCT AAACGACGCA CCACACCAAA CACAAAGAGA AGAAGAATCT	240
GAAGAGTTTT GTTATTCTTC ACCAAGTAAA CGGGTTGGAT CTTTCTCTAA TTCAAGCTCT	300
TCAGCTGTTG TTATCGAAGA TGGATCCGAT GACGATGAAC TTAACCGGGT CAGACCCAAT	360

AACCCACTTG TCACCCATCA GTTCTTCCCT GAGATGGATT CTAACGGCGG TGGTGTGCT 420
 TCTGGCTTTC CTCGGGCTCA CTGGTTTGGT GTTAAGTTTT GTCAGTCGGA TCTAGCCACC 480
 GGATCGTCCG CGGGTAAAGC TACCAACGTT GCCGCTGCCG TAGTGGAGCC GGCACAGCCG 540
 TTGAAAAAGA GTCGGCGTGG ACCAAGATCA AGAAGTTCTC AGTATAGAGG TGTTACGTTT 600
 TACCGGCGTA CCGGAAGATG GGAATCTCAT ATTTGGGACT GTGGGAAACA AGTTTACTTA 660
 GGTGGATTTG ACACTGCTCA TGCAGCAGCT CGAGCATATG ATAGAGCTGC TATTAAATTC 720
 CGTGGAGTAG AAGCGGATAT CAATTTCAAC ATCGACGATT ATGATGATGA CTTGAAACAG 780
 ATGACTAATT TAACCAAGGA AGAGTTCGTA CACGTACTTC GCCGACAAAG CACAGGCTTC 840
 CCTCGAGGAA GTTCGAAGTA TAGAGGTGTC ACTTTGCATA AGTGTGGTCG TTGGGAAGCT 900
 CGTATGGGTC AATTCTTAGG CAAAAGTAT GTTTATTTGG GTTTGTTCGA CACCGAGGTC 960
 GAAGCTGCTA GAGCTTACGA TAAAGCTGCA ATCAAATGTA ACGGCAAAGA CGCCGTGACC 1020
 AACTTTGATC CGAGTATTTA CGATGAGGAA CTCAATGCCG AGTCATCAGG GAATCCTACT 1080
 ACTCCACAAG ATCACAACCT CGATCTGAGC TTGGGAAATT CGGCTAATTC GAAGCATAAA 1140
 AGTCAAGATA TCGGCTCAG GATGAACCAA CAACAACAAG ATTCTCTCCA CTCTAATGAA 1200
 GTTCTTGGAT TAGGTCAAAC CGGAATGCTT AACCATACTC CCAATTCAA CCACCAATTT 1260
 CCGGGCAGCA GCAACATTGG TAGCGGAGGC GGATTCTCAC TGTTTCCGGC GGCTGAGAAC 1320
 CACCGGTTTG ATGGTCGGGC CTCGACGAAC CAAGTGTTGA CAAATGCTGC AGCATCATCA 1380
 GGATTCTCTC CTCATCATCA CAATCAGATT TTTAATTCTA CTTCTACTCC TCATCAAAT 1440
 TGGCTGCAGA CAAATGGCTT CCAACCTCCT CTCATGAGAC CTTCTTGAAT CTTTTATATT 1500
 TTTAAGGTTT ATTATTATAT AAGAAAAACA AAAATGAACC TTTGAAATCC CCACATGTTC 1560
 TTGGTCATTT CATTAAATCAT CGGCTTATAT TTTGCTTATT TTCCCCTAAA TCCTCTTGTT 1620
 AACTTAGGCG AACAAAAAAA ATTAATGGAA ATCTTTTCC CTCCATCGGT TACAAAAATA 1680

(2) INFORMATION FOR SEQ ID. NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..67
- (D) OTHER INFORMATION: /note= "AP2-R1 direct repeat at positions 129 to 195"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 32..49
- (D) OTHER INFORMATION: /note= "putative AP2-R1 amphipathic alpha-helix (SEQ ID NO:6)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ser Ser Gln Tyr Arg Gly Val Thr Phe Tyr Arg Arg Thr Gly Arg Trp
 1 5 10 15

Glu Ser His Ile Trp Asp Cys Gly Lys Gln Val Tyr Leu Gly Gly Phe
 20 25 30

Thr Asp Ala His Ala Ala Ala Arg Ala Tyr Asp Arg Ala Ala Ile Lys
 35 40 45

Phe Arg Gly Val Glu Ala Asp Ile Asn Phe Asn Ile Asp Asp Tyr Asp
 50 55 60

Asp Asp Leu
 65

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "AP2-R2 direct repeat at positions 221 to 288"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 33..50
- (D) OTHER INFORMATION: /note= "putative AP2-R2 amphipathic alpha-helix (SEQ ID NO:7)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ser Ser Lys Tyr Arg Gly Val Thr Leu His Lys Cys Gly Arg Trp Glu
 1 5 10 15

Ala Arg Met Gly Gln Phe Leu Gly Lys Lys Tyr Val Tyr Leu Gly Leu
 20 25 30

Phe Asp Thr Glu Val Glu Ala Ala Arg Ala Tyr Asp Lys Ala Ala Ile
 35 40 45

Lys Cys Asn Gly Lys Asp Ala Val Thr Asn Phe Asp Pro Ser Ile Tyr
 50 55 60
 Asp Glu Glu Leu
 65

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "putative AP2-R1 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Cl
cut Phe Asp Thr Ala His Ala Ala Ala Arg Ala Tyr Asp Arg Ala Ala Ile
 1 5 10 15
 Lys Phe

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "putative AP2-R2 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Phe Asp Thr Glu Val Glu Ala Ala Arg Ala Tyr Asp Lys Ala Ala Ile
 1 5 10 15
 Lys Cys

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Arg Ala Tyr Asp
 1

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

C1
C14
 (ix) FEATURE:

- (A) NAME/KEY: Peptide
 (B) LOCATION: 1..77
 (D) OTHER INFORMATION: /note= "ANT-R1 direct repeat"

(ix) FEATURE:

- (A) NAME/KEY: Region
 (B) LOCATION: 44..59
 (D) OTHER INFORMATION: /note= "putative ANT-R1 amphipathic
 alpha-helix (SEQ ID NO:37)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Thr	Ser	Gln	Tyr	Arg	Gly	Val	Thr	Arg	His	Arg	Trp	Thr	Gly	Arg	Tyr	1	5	10	15
Glu	Ala	His	Leu	Trp	Asp	Asn	Ser	Phe	Lys	Lys	Glu	Gly	His	Ser	Arg	20	25	30	
Lys	Gly	Arg	Gln	Val	Tyr	Leu	Gly	Gly	Tyr	Asp	Met	Glu	Glu	Lys	Ala	35	40	45	
Ala	Arg	Ala	Tyr	Asp	Leu	Ala	Ala	Leu	Lys	Tyr	Trp	Gly	Pro	Ser	Thr	50	55	60	
His	Thr	Asn	Phe	Ser	Ala	Glu	Asn	Tyr	Gln	Lys	Glu	Ile	65	70	75				

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: /note= "ANT-R2 direct repeat"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 37..51
- (D) OTHER INFORMATION: /note= "putative ANT-R2 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala Ser Ile Tyr Arg Gly Val Thr Arg His His Gln His Gly Arg Trp
 1 5 10 15

Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly
 20 25 30

Thr Phe Gly Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp Val Ala Ala
 35 40 45

Ile Lys Phe Arg Gly Thr Asn Ala Val Thr Asn Phe Asp Ile Thr Arg
 50 55 60

Tyr Asp Val Asp Arg
 65

Cl
Cmt

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..67
- (D) OTHER INFORMATION: /note= "RAP2.7-R1 direct repeat"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 33..49
- (D) OTHER INFORMATION: /note= "putative RAP2.7-R1 amphipathic alpha helix (SEQ ID NO:36)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ser Ser Gln Tyr Arg Gly Val Thr Phe Tyr Arg Arg Thr Gly Arg Trp
 1 5 10 15

Glu Ser His Ile Trp Asp Cys Gly Lys Gln Val Tyr Leu Gly Gly Phe
 20 25 30

Asp Thr Ala His Ala Ala Ala Arg Ala Tyr Asp Arg Ala Ala Ile Lys
 35 40 45

Phe Arg Gly Val Asp Ala Asp Ile Asn Phe Thr Leu Gly Asp Tyr Glu
 50 55 60

Glu Asp Met
 65

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..53
- (D) OTHER INFORMATION: /note= "RAP2.7-R2 direct repeat"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 26..34
- (D) OTHER INFORMATION: /note= "putative RAP2.7-R2 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser Ser Lys Tyr Arg Gly Val Thr Leu His Lys Cys Gly Arg Trp Glu
 1 5 10 15

Ala Arg Met Gly Gln Phe Leu Gly Lys Lys Ala Tyr Asp Lys Ala Ala
 20 25 30

Ile Asn Thr Asn Gly Arg Glu Ala Val Thr Asn Phe Glu Met Ser Ser
 35 40 45

Tyr Gln Asn Glu Ile
 50

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Tyr Arg Gly Val Thr
1 5

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ala or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Arg or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Gly Arg Trp Glu Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Val Tyr Leu Gly
1

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ala Ala Ile Lys
1

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
 (B) LOCATION: 1..69
 (D) OTHER INFORMATION: /note= "AP2 domain within tobacco EREBP-1"

(ix) FEATURE:

- (A) NAME/KEY: Region
 (B) LOCATION: 36..51
 (D) OTHER INFORMATION: /note= "putative EREBP-1 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Gly Arg His Tyr Arg Gly Val Arg Arg Arg Pro Trp Gly Lys Phe Ala
1 5 10 15
Ala Glu Ile Arg Asp Pro Ala Lys Asn Gly Ala Arg Val Trp Leu Gly
20 25 30
Thr Tyr Glu Thr Asp Glu Glu Ala Ala Ile Ala Tyr Asp Lys Ala Ala
35 40 45
Tyr Arg Met Arg Gly Ser Lys Ala His Leu Asn Phe Pro Leu Glu Val
50 55 60

Ala Asn Phe Lys Gln
65

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1..69
 (D) OTHER INFORMATION: /note= "AP2 domain within tobacco EREBP-2"

- (ix) FEATURE:
 (A) NAME/KEY: Region
 (B) LOCATION: 35..51
 (D) OTHER INFORMATION: /note= "putative EREBP-2 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

C1
Cont

Gly	Arg	His	Tyr	Arg	Gly	Val	Arg	Gln	Arg	Pro	Trp	Gly	Lys	Phe	Ala
1				5				10						15	
Ala	Glu	Ile	Arg	Asp	Pro	Ala	Lys	Asn	Gly	Ala	Arg	Val	Trp	Leu	Gly
			20				25						30		
Thr	Tyr	Glu	Thr	Ala	Glu	Glu	Ala	Ala	Leu	Ala	Tyr	Asp	Lys	Ala	Ala
		35					40					45			
Tyr	Arg	Met	Arg	Gly	Ser	Lys	Ala	Leu	Leu	Asn	Phe	Pro	His	Arg	Ile
		50				55					60				
Gly	Leu	Asn	Glu	Pro											
65															

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "AP2 domain within tobacco EREBP-3"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 35..50
- (D) OTHER INFORMATION: /note= "putative EREBP-3 amphipathic alpha-helix (SEQ ID NO:41)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Glu Val His Tyr Arg Gly Val Arg Lys Arg Pro Trp Gly Arg Tyr Ala
1 5 10 15

Ala Glu Ile Arg Asp Pro Gly Lys Lys Ser Arg Val Trp Leu Gly Thr
20 25 30

Phe Asp Thr Ala Glu Glu Ala Ala Lys Ala Tyr Asp Thr Ala Ala Arg
35 40 45

Glu Phe Arg Gly Pro Lys Ala Lys Thr Asn Phe Pro Ser Pro Thr Glu
50 55 60

Asn Gln Ser Pro
65

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: /note= "AP2 domain within tobacco EREBP-4"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 35..51
- (D) OTHER INFORMATION: /note= "putative EREBP-4 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Lys Lys His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Phe Ala
1 5 10 15

Ala Glu Ile Arg Asp Pro Asn Arg Lys Gly Thr Arg Val Trp Leu Gly
 20 25 30

Thr Phe Asp Thr Ala Ile Glu Ala Ala Lys Ala Tyr Asp Arg Ala Ala
 35 40 45

Phe Lys Leu Arg Gly Ser Lys Ala Ile Val Asn Phe Pro His Arg Ile
 50 55 60

Gly Leu Asn Glu Pro
 65

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis
 RAP2.2 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 34..51
- (D) OTHER INFORMATION: /note= "putative RAP2.2 amphipathic
 alpha-helix (SEQ ID NO:38)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Lys Asn Gln Tyr Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp Ala
 1 5 10 15

Ala Glu Ile Arg Asp Pro Arg Lys Gly Ser Arg Glu Trp Leu Gly Thr
 20 25 30

Phe Asp Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Ala Ala Ala Arg
 35 40 45

Arg Ile Arg Gly Thr Lys Ala Lys Val Asn Phe Pro Glu Glu Lys Asn
 50 55 60

Pro Ser Val Val
 65

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis RAP2.3 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 36..50
- (D) OTHER INFORMATION: /note= "putative RAP2.3 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Lys Asn Val Tyr Arg Gly Ile Arg Lys Arg Pro Trp Gly Lys Trp Ala
 1 5 10 15
 Ala Glu Ile Arg Asp Pro Arg Lys Gly Val Arg Val Trp Leu Gly Thr
 20 25 30
 Phe Asn Thr Ala Glu Glu Ala Ala Met Ala Tyr Asp Val Ala Ala Lys
 35 40 45
 Gln Ile Arg Gly Asp Lys Ala Lys Leu Asn Phe Pro Asp Leu His His
 50 55 60
 Pro Pro Pro Pro
 65

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis RAP2.5 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 35..50
- (D) OTHER INFORMATION: /note= "putative RAP2.5 amphipathic alpha-helix (SEQ ID NO:39)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Glu Ile Arg Tyr Arg Gly Val Arg Lys Arg Pro Trp Gly Arg Tyr Ala
 1 5 10 15
 Ala Glu Ile Arg Asp Pro Gly Lys Lys Thr Arg Val Trp Leu Gly Thr
 20 25 30
 Phe Asp Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Thr Ala Ala Arg
 35 40 45
 Asp Phe Arg Gly Ala Lys Ala Lys Thr Asn Phe Pro Thr Phe Leu Glu
 50 55 60
 Leu Ser Asp Gln
 65

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis RAP2.6 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 34..51
- (D) OTHER INFORMATION: /note= "putative RAP2.6 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Pro Lys Lys Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Trp Ala
 1 5 10 15
 Ala Glu Ile Arg Asp Pro His Lys Ala Thr Arg Val Trp Leu Gly Thr
 20 25 30
 Phe Glu Thr Ala Glu Ala Ala Ala Arg Ala Tyr Asp Ala Ala Ala Leu
 35 40 45

Arg Phe Arg Gly Ser Lys Ala Lys Leu Asn Phe Pro Glu Asn Val Gly
 50 55 60
 Thr Gln Thr Ile
 65

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis
RAP2.12 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 34..51
- (D) OTHER INFORMATION: /note= "putative RAP2.12 amphipathic
alpha-helix (SEQ ID NO:40)"

Cl
 nly

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Lys Asn Gln Tyr Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp Ala
 1 5 10 15
 Ala Glu Ile Arg Asp Pro Arg Glu Gly Ala Arg Ile Trp Leu Gly Thr
 20 25 30
 Phe Lys Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Ala Ala Ala Arg
 35 40 45
 Arg Ile Arg Gly Ser Lys Ala Lys Val Asn Phe Pro Glu Glu Asn Met
 50 55 60
 Lys Ala Asn Ser
 65

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis TINY AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 35..50
- (D) OTHER INFORMATION: /note= "putative TINY amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

His Pro Val Tyr Arg Gly Val Arg Lys Arg Asn Trp Gly Lys Trp Val
1 5 10 15

Ser Glu Ile Arg Glu Pro Arg Lys Lys Ser Arg Ile Trp Leu Gly Thr
20 25 30

Phe Pro Ser Pro Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu
35 40 45

Ser Ile Lys Gly Ala Ser Ala Ile Leu Asn Phe Pro Asp Leu Ala Gly
50 55 60

Ser Phe Pro Arg
65

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis RAP2.1 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 35..50
- (D) OTHER INFORMATION: /note= "putative RAP2.1 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Arg Lys Pro Tyr Arg Gly Ile Arg Arg Arg Lys Trp Gly Lys Trp Val
1 5 10 15

Ala Glu Ile Arg Glu Pro Asn Lys Arg Ser Arg Leu Trp Leu Gly Ser
 20 25 30

Tyr Thr Thr Asp Ile Ala Ala Ala Arg Ala Tyr Asp Val Ala Val Phe
 35 40 45

Tyr Leu Arg Gly Pro Ser Ala Arg Leu Asn Phe Pro Asp Leu Leu Leu
 50 55 60

Gln Glu Glu Asp
 65

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis
RAP2.4 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 35..50
- (D) OTHER INFORMATION: /note= "putative RAP2.4 amphipathic
alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Thr Lys Leu Tyr Arg Gly Val Arg Gln Arg His Trp Gly Lys Trp Val
 1 5 10 15

Ala Glu Ile Arg Leu Pro Arg Asn Arg Thr Arg Leu Trp Leu Gly Thr
 20 25 30

Phe Asp Thr Ala Glu Glu Ala Ala Leu Ala Tyr Asp Lys Ala Ala Tyr
 35 40 45

Lys Leu Arg Gly Asp Phe Ala Arg Leu Asn Phe Pro Asn Leu Arg His
 50 55 60

Asn Gly Phe His
 65

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide


(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..66
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis RAP2.8 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 33..48
- (D) OTHER INFORMATION: /note= "putative RAP2.8 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:


 Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly
 1 5 10 15
 Ala Gln Ile Tyr Glu Lys His Gln Arg Val Trp Leu Gly Thr Phe Asn
 20 25 30
 Glu Gln Glu Glu Ala Ala Arg Ser Tyr Asp Ile Ala Ala Cys Arg Phe
 35 40 45
 Arg Gly Arg Asp Ala Val Val Asn Phe Lys Asn Val Leu Glu Asp Gly
 50 55 60
 Asp Leu
 65

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis RAP2.10 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 36..51
- (D) OTHER INFORMATION: /note= "putative RAP2.10
amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```

Asp Lys Pro Tyr Lys Gly Ile Arg Met Arg Lys Trp Gly Lys Trp Val
1           5           10           15
Ala Glu Ile Arg Glu Pro Asn Lys Arg Ser Arg Ile Trp Leu Gly Ser
          20           25           30
Tyr Ser Thr Pro Glu Ala Ala Ala Arg Ala Tyr Asp Thr Ala Val Phe
          35           40           45
Tyr Leu Arg Gly Pro Ser Ala Arg Leu Asn Phe Pro Glu Leu Leu Ala
          50           55           60
Gly Val Thr Val
65

```

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

*Cl
unit*

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis
RAP2.11 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 34..50
- (D) OTHER INFORMATION: /note= "putative RAP2.11
amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```

Lys Thr Lys Phe Val Gly Val Arg Gln Arg Pro Ser Gly Lys Trp Val
1           5           10           15
Ala Glu Ile Lys Asp Thr Thr Gln Lys Ile Arg Met Trp Leu Gly Thr
          20           25           30
Phe Glu Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Glu Ala Ala Cys
          35           40           45

```

Leu Leu Arg Gly Ser Asn Thr Arg Thr Asn Phe Ala Asn His Phe Pro
 50 55 60
 Asn Asn Ser Gln
 65

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 4
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Val or Ile"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Cl
cut
 Tyr Arg Gly Xaa Arg
 1 5

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 3
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = positively charged
 amino acid"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 4
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Trp, Phe or Tyr"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 5
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Ala or Val"

Clut

(A) NAME/KEY: Modified-site
(B) LOCATION: 9
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Arg or Lys"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 10
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Asp or Glu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Trp Gly Xaa Xaa Xaa Ala Glu Ile Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 4
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ser or Thr"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 5
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Tyr or Phe"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Trp Leu Gly Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ile, Leu or positively
charged amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Glu Glu Ala Ala Xaa Ala Tyr Asp
1 5


(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- 
- (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..17
 - (D) OTHER INFORMATION: /note= "putative RAP2.7-R1
amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Asp Thr Ala His Ala Ala Ala Arg Ala Tyr Asp Arg Ala Ala Ile Lys
1 5 10 15
Phe

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "putative ANT-R1 amphipathic
alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Glu Glu Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "putative RAP2.2 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Cl
 Asp Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Ala Ala Ala Arg Arg
 1 5 10 15
ant
 Ile Arg

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "putative RAP2.5 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Thr Ala Ala Arg Asp Phe
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "putative RAP2.12
amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Lys Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Ala Ala Ala Arg Arg
 1 5 10 15

Ile Arg

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "putative EREBP-3
amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Thr Ala Glu Glu Ala Ala Lys Ala Tyr Asp Thr Ala Ala Arg Glu Phe
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "AP2 linker region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Lys Gln Met Thr Asn Leu Thr Lys Glu Glu Phe Val His Val Leu Arg
 1 5 10 15

Arg Gln Ser Thr Gly Phe Pro Arg Gly
 20 25

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "ANT linker region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Glu Asp Met Met Lys Asn Met Thr Arg Gln Glu Tyr Val Ala His Leu
 1 5 10 15

Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly
 20 25

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "RAP2.7 linker region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met	Lys	Gln	Val	Gln	Asn	Leu	Ser	Lys	Glu	Glu	Phe	Val	His	Ile	Leu
1				5					10					15	
Arg	Arg	Gln	Ser	Thr	Gly	Phe	Ser	Arg	Gly						
			20					25							

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = positively charged
amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Asn	Leu	Thr	Xaa	Glu	Glu	Phe	Val	His
1				5				

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Leu	Arg	Arg	Gln	Ser	Thr	Gly	Phe	Ser	Arg	Gly
1				5					10	

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "JOAP2U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GTTGCCGCTG CCGTAGTG

18


(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- 
- (A) NAME/KEY: -
 - (B) LOCATION: 1..22
 - (D) OTHER INFORMATION: /note= "JOAP2L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GGTTCATCCT GAGCCGCATA TC

22

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /note= "JORAP2.1U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTCAAGAAGA AGTGCCTAAC CACG

24

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JORAP2.1L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GCAGAAGCTA GAAGAGCGTC GA

22

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "JORAP2.2U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGAAAATGGG CTGCGGAG

18

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JORAP2.2L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GTTACCTCCA GCATCGAACG AG

22

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JORAP2.4U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GCTGGATCTT GTTTCGCTTA CG

22

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- CIA*
Cart
- (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JORAP2.4L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GCTTCAAGCT TAGCGTCGAC TG

22

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "JORAP2.5U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

AGATGGGCTT GAAACCCGAC

20

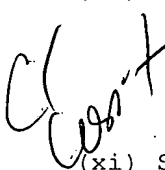
(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- 
- (A) NAME/KEY: -
 - (B) LOCATION: 1..18
 - (D) OTHER INFORMATION: /note= "JORAP2.5L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CTGGCTAGGG CTACGCGC

18

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JORAP2.6U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TTCTTTGCCT CCTCAACCAT TG

22

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JORAP2.6L primer"


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

TCTGAGTTCC AACATTTTCG GG

22

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- 
- (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JORAP2.7U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GAAATTGGTA ACTCCGGTTC CG

22

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JORAP2.7L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CCATTTTGCT TTGGCGCATT AC

22

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "JORAP2.8U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GGCGTTACGC CTCTACCGG

19

(2) INFORMATION FOR SEQ ID NO:62:

- cl*
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "JORAP2.8L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CGCCGTCTTC CAGAACGTTT

20

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "JORAP2.9U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ATCACGGATC TGGCTTGGTT C

21

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JORAP2.9L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GCCTTCTTCC GTATCAACGT CG

22

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "JORAP2.10U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GTCAACTCCG GCGGTTACG

19

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "JORAP2.10L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

TCTCCTTATA TACGCCGCCG A

21

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "JORAP2.11U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GAGAAGAGCA AAGGCAACAA GAC

23

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "JORAP2.11L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

AGTTGTTAGG AAAATGGTTT GCG

23

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:


- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "JORAP2.12U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

AAACCATTCG TTTTCACTTC GACTC

25

(2) INFORMATION FOR SEQ ID NO:70:

- 
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "JORAP2.12L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

TCACAGAGCG TTTCTGAGAA TTAGC

25

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "AP2U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

ATGTGGGATC TAAACGACGC AC

22

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "AP2L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GATCTTGGTC CACGCCGAC

19

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.1U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

AAGAGGACCA TCTCTCAG

18

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..18
 - (D) OTHER INFORMATION: /note= "RAP2.1L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

AACACTCGCT AGCTTCTC

18

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..18
 - (D) OTHER INFORMATION: /note= "RAP2.2U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

TGGTTCAGCA GCCAACAC

18

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..19
 - (D) OTHER INFORMATION: /note= "RAP2.2L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

CAATGCATAG AGCTTGAGG

19

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:


- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.4U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

ACGGATTTCA CATCGGAG

18

(2) INFORMATION FOR SEQ ID NO:78:

- 
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA .

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "RAP2.4L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CTAAGCTAGA ATCGAATCC

19

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.5U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TACCGGTTTC GCGCGTAG

18

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "RAP2.5L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CACCTTCGAA ATCAACGACC G

21

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "RAP2.6U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TTCCCCGAAA ATGTTGGAAC TC

22

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "RAP2.6L primer"


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

TGGGAGAGAA AAAATTGGTA GATCG

25

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- 
- (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.7U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CGATGGAGAC GAAGACTC

18

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.7L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GTCGGAACCG GAGTTACC

18

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "RAP2.8U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TCACTCAAAG GCCGAGATC

19

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "RAP2.8L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

TAACAACATC ACCGGCTCG

19

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.9U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GTGAAGGCTT AGGAGGAG

18


(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- 
- (A) NAME/KEY: -
 - (B) LOCATION: 1..19
 - (D) OTHER INFORMATION: /note= "RAP2.9L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

TGCCTCATAT GAGTCAGAG

19

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.10U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

TCCCGGAGCT TTTAGCCG

18

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:


- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "RAP2.10L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CAACCCGTTC CAACGATCC

19

(2) INFORMATION FOR SEQ ID NO:91:

- 
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "RAP2.11U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TTCTTCACCA GAAGCAGAGC ATG

23

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /note= "RAP2.11L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CTCCATTGAT TGCATATAGG GACG

24

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /note= "RAP2.12U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GCTTTGGTTC AGAACTCGAA CATC

24

(2) INFORMATION FOR SEQ ID NO:94:

- C1*
ant
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "RAP2.12L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

AGGTTGATAA ACGAACGATG CG

22

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Lys Lys Ser Arg
1

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..18
 (D) OTHER INFORMATION: /note= "RAP2.3 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

TCATCGCCAC GATCAACC

18

(2) INFORMATION FOR SEQ ID NO:97:

- C114*
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..18
 (D) OTHER INFORMATION: /note= "RAP2.3 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

AGCAGTCCAA TGCGACGG

18

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Trp Ala Ala Glu Ile Arg Asp
1 5

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Met Ala Asp Ser
1

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 729 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..729
 (D) OTHER INFORMATION: /note= "RAP2.1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GAAGAGTCTA CGATGAGAAA GAGAAGGCAG CCACCTCAAG AAGAAGTGCC TAACCACGTG	60
GCTACAAGGA AGCCGTACAG AGGGATACGG AGGAGGAAGT GGGGCAAGTG GGTGGCTGAG	120
ATTCGTGAGC CTAACAAACG CTCACGGCTT TGGCTTGGCT CTTACACAAC CGATATCGCC	180
GCCGCTAGAG CCTACGACGT GGCCGTCTTC TACCTCCGTG GCCCCTCCGC ACGTCTCAAC	240
TTCCCTGATC TTCTCTTGCA AGAAGAGGAC CATCTCTCAG CCGCCACCAC CGCTGACATG	300
CCCCGAGCTC TTATAAGGGA AAAAGCGGCG GAGGTCGGCG CCAGAGTCGA CGCTCTTCTA	360
GCTTCTGCCG CTCCTTCGAT GGCTCACTCC ACTCCGCCGG TAATAAAACC CGACTTGAAT	420
CAAATACCCG AATCCGGAGA TATATAGTCA ATTTATATAC ATGTAGTTTG TTTTGTTTGA	480
TTAGAAGATT ACATTTACAT ACAAGATACA CATAGATACT GGAAAATATA GGTATGTATA	540
CATTCATAAA TTATCTTATG TATCAAAGAA TTTTATAGAT TCTGATTAGC TTTTGTGTTT	600

TGTTTTTGAT AAGAACTCTG ATTAGTTGTC CGGAGACAAA ACCGGCTAAG AGCAATCCAT	660
GAGAAGCTAG CGAGTGTTTT TTAGTTCAAG TTGTAATATA AATGCATATT AATTCTTTAG	720
TAATTTTGT	729

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1101
- (D) OTHER INFORMATION: /note= "RAP2.2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

CGTCCTTGGG GAAAATGGGC TCGGAGATC CGTGATCCGA GAAAAGGCTC CCGAGAATGG	60
CTTGGAACAT TCGACACTGC TGAGGAAGCA GCAAGAGCTT ATGATGCTGC AGCACGCAGA	120
ATCCGTGGCA CGAAAGCTAA GGTGAATTTT CCCGAGGAGA AGAACCCTAG CGTCGTATCC	180
CAGAAACGTC CTAGTGCTAA GACTAATAAT CTTCAGAAAT CAGTGGCTAA ACCAAACAAA	240
AGCGTAACTT TGGTTCAGCA GCCAACACAT CTGAGTCAGC AGTACTGCAA CAACTCCTTT	300
GACAACTCTT TTGGTGATAT GAGTTTCATG GAAGAGAAGC CTCAGATGTA CAACAATCAG	360
TTTGGGTAA CAACTCGTT CGATGCTGGA GGTAACAATG GATACCAGTA TTTAGTTCC	420
GATCAGGGCA GTAACCTCTT CGACTGTTCT GAGTTCGGGT GGAGTGATCA CGGCCCTAAA	480
ACACCCGAGA TCTCTTCAAT GCTTGTCAT AACAACGAAG CATCATTTGT TGAAGAAACC	540
AATGCAGCCA AGAAGCTCAA ACCAACTCT GATGAGTCAG ACGATCTGAT GGCATACCTT	600
GACAACGCCT TGTGGGACAC CCCACTAGAA GTGGAAGCCA TGCTTGGCGC AGATGCTGGT	660
GCTGTGACTC AGGAAGAGGA AAACCCAGTG GAGCTATGGA GCTTAGATGA GATCAATTTT	720
ATGCTGGAAG GAGACTTTTG AAGTGATCGA TGGTTCCTTA GTTTGTAAAT AAAGCTGTGT	780
TGGATTTTGC TGTGGGGGA TGGTACAAGT CACACCTCAA GCTCTATGCA TTGGTATCTC	840
ATGAGCCTTC TCTTCCATAG AGAGTTTCTC TTTAATTTT GTCGAAATAA AAAAGGTGTG	900
ATGAAGTAAA TAGAGGTATA ATAATATCTA TCTATTAAGT CTTGTTTTGT TCTTTCATTT	960
TTGTATTTCT TTTCTATTTA AAAGACAGTT TATTAGTCTT CTGAGCTCTC TTTTGTATCT	1020
TTGTTATAGC GTATCATCAC CCTCGAAAGT GTAATGTTTT GTACCCCAA ACTTGTTTAG	1080

CATTATAATA AAGTCTCTTT G

1101

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1055 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1055
- (D) OTHER INFORMATION: /note= "RAP2.3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

ATAAAGGCAT TTCAGCTCCA CCGTAGGAAA CTTTCTCTTG AAAGAAACCC ACAGCAACAA 60

ACAGAGAAAA TGTGTGGCGG TGCTATTATT TCCGATTATG CCCCTCTCGT CACCAAGGCC 120

AAGGGCCGTA AACTCACGGC TGAGGAACTC TGGTCAGAGC TCGATGCTTC CGCCGCCGAC 180

GACTTCTGGG GTTTCTATTC CACCTCCAAA CTCCATCCCA CCAACCAAGT TAACGTGAAA 240

GAGGAGGCAG TGAAGAAGGA GCAGGCAACA GAGCCGGGGA AACGGAGGAA GAGGAAGAAT 300

GTTTATAGAG GGATACGTAA GCGTCCATGG GGAAAAATGGG CGGCTGAGAT TCGAGATCCA 360

CGAAAAAGTG TTAGAGTTTG GCTTGGTACG TTCAACACGG CGGAGGAAGC TGCCATGGCT 420

TATGATGTTG CGGCCAAGCA GATCCGTGGT GATAAAGCCA AGCTCAACTT CCCAGATCTG 480

CACCATCCTC CTCCTCCTAA TTATACTCCT CCGCCGTCAT CGCCACGATC AACCGATCAG 540

CCTCCGGCGA AGAAGGTCTG CGTTGTCTCT CAGAGTGAGA GCGAGTTAAG TCAGCCGAGT 600

TTCCCGGTGG AGTGTATAGG ATTTGGAAAT GGGGACGAGT TTCAGAACCT GAGTTACGGA 660

TTTGAGCCGG ATTATGATCT GAAACAGCAG ATATCGAGCT TGGAAATCGTT CCTTGAGCTG 720

GACGGTAACA CGGCGGAGCA ACCGAGTCAG CTTGATGAGT CCGTTTCCGA GGTGGATATG 780

TGGATGCTTG ATGATGTCAT TGCCTCGTAT GAGTAAAAGA AAAAAAATAA GTTTAAAAAA 840

AGTTAAATAA AGTCTGTAAT ATATATGTAA CCGCCGTTAC TTTTAAAAGG TTTTACCGT 900

CGCATTGGAC TGCTGATGAT GTCTGTTGTG TAATGTGTAG AATGTGACCA AATGGACGTT 960

ATATTACGGT TTGTGGTATT ATTAGTTTCT TAGATGGAAA AACTTACATG TGTAATAAAG 1020

ATTTGTAATG TAAGACGAAG TACTTATAAC TTCTT 1055

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 969 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- cl*
wt (A) NAME/KEY: -
 (B) LOCATION: 1..969
 (D) OTHER INFORMATION: /note= "RAP2.4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

```

TCTTCCTCCG ACGCATCACA ACAACAACAA CTCTTTCTCG AATCTTCTCA GCCCAAAGCC      60
GTTACTGATG AAGCAATCTG GAGTCGCTGG ATCTTGTTTC GCTTACGGTT CAGGTGTTCC      120
TTCGAAGCCG ACGAAGCTTT ACAGAGGTGT GAGGCAACGT CACTGGGGAA AATGGGTGGC      180
TGAGATCCGT TTGCCGAGAA ATCGGACTCG TCTCTGGCTT GGGACTTTTG ACACGGCGGA      240
GGAAGCTGCG TTGGCCTATG ATAAGGCGGC GTACAAGCTG CGCGGCGATT TCGCCCGGCT      300
TAACTTCCCT AACCTACGTC ATAACGGATT TCACATCGGA GCGGATTTTC GTGAATATAA      360
ACCTCTTCAC TCCTCAGTCG ACGCTAAGCT TGAAGCTATT TGTAAGCA TGGCGGAGAC      420
TCAGAAACAG GACAAATCGA CGAAATCATC GAAGAAACGT GAGAAGAAGG TTTCGTCGCC      480
AGATCTATCG GAGAAAGTGA AGGCGGAGGA GAATTCGGTT TCGATCGGTG GATCTCCACC      540
GGTGACGGAG TTTGAAGAGT CCACCGCTGG ATCTTCGCCG TTGTCGGACT TGACGTTTCG      600
TGACCCGGAG GAGCCGCCGC AGTGGAACGA GACGTTCTCG TTGGAGAAGT ATCCGTCGTA      660
CGAGATCGAT TGGGATTCGA TTCTAGCTTA GGGGCAAAAT AGGAAATTCA GCCGCTTGCA      720
ATGGAGTTTT TGTGAAATTG CATGACTGGC CCAAGAGTAA TTAATTAAAT ATGGATTAGT      780
GTAAATTTTC GTATGTTAAT ATTTGTATTA TGGTTTGAT TAGTCTCTCT GTGTCGGTCC      840
AGCTTGCGGT TTTTGTGTCAG GCTCGACCAT GCCACAGTTT TCATTTTATG TAATCTTTTT      900
TTCTTTTGTC TTATGTAATT TGTAGCTTCA GTTCTTCAT CTATAATGCA ATTTTATTAT      960
GATTATGTG

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(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 937 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..937

(D) OTHER INFORMATION: /note= "RAP2.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```

GTCGACCCAC GCGTCCGACT CTCTCTCTAA TCTATCTATC CGAGAATGGC CAAGATGGGC      60
TTGAAACCCG ACCCGGCTAC TACTAACCAG ACCCACAATA ATGCCAAGGA GATTCGTTAC      120
AGAGGCGTTA GGAAGCGTCC TTGGGGCCGT TATGCCGCCG AGATCCGAGA TCCGGGCAAG      180
AAAACCCGCG TCTGGCTTGG CACTTTCGAT ACGGCTGAAG AGGCGGCGCG TGCTTACGAT      240
ACGGCGGCGC GTGATTTTCG TGGTGCTAAG GCTAAGACCA ATTTCCCAAC TTTTCTCGAG      300
CTGAGTGACC AGAAGGTCCC TACCGGTTTC GCGCGTAGCC CTAGCCAGAG CAGCACGCTC      360
GACTGTGCTT CTCCTCCGAC GTTAGTTGTG CCTTCAGCGA CGGCTGGGAA TGTTCCCCCG      420
CAGCTCGAGC TTAGTCTCGG CGGAGGAGGC GCGGCTCGT GTTATCAGAT CCCGATGTCG      480
CGTCCTGTCT ACTTTTTTGA CCTGATGGGG ATCGGTAACG TAGGTCGTGG TCAGCCTCCT      540
CCTGTGACAT CGGCGTTTAG ATCGCCGGTG GTGCATGTTG CGACGAAGAT GGCTTGTGGT      600
GCCCCAAGCG ACTCTGATTC GTCATCGGTC GTTGATTTTC AAGGTGGGAT GGAGAAGAGA      660
TCTCAGACTG TTAGATCTAG ATCTTAATTT GCCTCCTCCA TCGGAACAGG CCTGAGCTTT      720
TAACGGTGTC GTTTC AATTC GAAGCGCATG CGTTTCTTCT TCTTTTGTAG CTGTGAAAAT      780
TCGTTTTTCTC ATAGTTTTTC CTCTCTCTCT CTCTCAGTCT AAATTTATTA CCAGTTTTTA      840
GAAAGAAAAA ACAGATTAAA TCTGAGAGAG AAAAATATAA TTTTAGCTGA CATGGATCGT      900
TATGTACATA TTATTACATA ACCGGAGATC TGAAC TG      937

```

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 651 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..651

(D) OTHER INFORMATION: /note= "RAP2.6"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

AAGAGAAGAG TTTTCTTTGC CTCCTCAACC ATTGATTACC GGTTCAGCTG TGAATAAAGA	60
ATGTGAAAGC TCAATGTCCT TGGAGAGGCC AAAAAAATAT AGAGGAGTAA GGCAACGACC	120
ATGGGGAAAA TGGGCGGCGG AGATTCGAGA CCCACACAAG GCGACACGTG TATGGCTTGG	180
GACATTCGAG ACAGCCGAGG CCGCCGCAAG AGCCTATGAT GCGGCAGCAC TTCGCTTTAG	240
AGGAAGCAAA GCAAAGCTTA ATTTCCCCGA AAATGTTGGA ACTCAGACGA TTCAACGAAA	300
TTCTCATTTT TTGCAAACT CAATGCAACC TTCTCTAACA TACATCGATC AATGTCCAAC	360
TCTATTATCT TACTCTCGAT GTATGGAGCA ACAACAACCA TTAGTAGGCA TGTTGCAGCC	420
AACAGAAGAG GAAAATCACT TTTTCGAAAA ACCATGGACC GAATATGATC AATACAATTA	480
CTCCTCTTTT GGTAACTAA CATATCGTCA ACGCTTTGTA TTTCTACTTA TTCGATCTAC	540
CAATTTTTTC TCTCCAATA CAACTTCAGT CTGATTATTG CCTTCTTAGA TATGTCTTCG	600
AATGTTATGA CTATACATGG GTGTATATAA AATTTGTGAT CAAAGTCTTG T	651

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: -
 (B) LOCATION: 1..1329
 (D) OTHER INFORMATION: /note= "RAP2.7"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

AATGCCGATG GAGACGAAGA CTCTTGCTCT ACTCGAGCTT TCACTCTCAG TTTCGATATT	60
TTAAAAGTCG GAAGTAGTAG CGGCGGAGAC GAAAGCCCCG CCGCTTCAGC TTCCGTTACT	120
AAAGAGTTTT TTCCGGTGAG TGGAGACTGT GGACATCTAC GAGATGTTGA AGGATCATCA	180
AGCTCTAGAA ACTGGATAGA TCTTTCTTTT GACCGTATTG GTGACGGAGA AACGAAATTG	240
GTAAGTCCGG TTCCGACTCC GGCTCCGGTT CCGGCTCAGG TAAAAAGAG TCGGAGAGGA	300
CCAAGGTCTA GAAGTTCACA GTATAGAGGA GTTACTTTTT ATAGAAGAAC TGGTCGATGG	360
GAGTCACATA TTTGGGATTG TGGGAAACAA GTTTATTTAG GTGGTTTCGA CACTGCTCAT	420
GCTGCAGCTA GAGCTTATGA TCGAGCTGCT ATTAAATTTA GAGGTGTTGA TGCTGATATC	480
AACTTTACTC TTGGTGATTA TGAGGAAGAT ATGAAACAGG TACAAAACCTT GAGTAAGGAA	540

GAGTTTGTGC ATATACTGCG TAGACAGAGC ACGGGGTTTT CGCGGGGGAG TTCGAAGTAT	600
CGAGGGGTTA CGTTACACAA ATGTGGTAGA TGGGAAGCTA GGATGGGGCA GTTCTTGGT	660
AAAAAGGCTT ATGACAAGGC TGCAATCAAC ACTAATGGTA GAGAAGCAGT CACGAACTTC	720
GAGATGAGTT CATAACAAA TGAGATTAAC TCTGAGAGCA ATAACTCTGA GATTGACCTC	780
AACTTGGGAA TCTCTTTATC GACCGGTAAT GCGCCAAAGC AAAATGGGAG GCTCTTTCAC	840
TTCCCTTCTA ATACTTATGA AACTCAGCGT GGAGTTAGCT TGAGGATAGA TAACGAATAC	900
ATGGGAAAGC CGGTGAATAC ACCTCTTCCT TATGGATCCT CGGATCATCG CCTTTACTGG	960
AACGGAGCAT GCCCGAGTTA TAATAATCCC GCCGAGGGAA GAGCAACAGA AAAGAGAAGT	1020
GAAGCTGAAG GGATGATGAG TAACTGGGGA TGGCAGAGAC CGGGGCAAAC AAGCGCCGTG	1080
AGACCGCAGC CACCGGGACC ACAACCACCA CCATTGTTCT CAGTTGCAGC AGCATCATCA	1140
GGATTCTCAC ATTTCCGGCC ACAACCTCCC AATGACAATG CAACACGTGG TTACTIONTAT	1200
CCACACCCTT AACTTGTAAG GGGACATATG AGAGTTTTTT TACCATCTCT CTCTCTCTCA	1260
AACTCTAGT CCCCTTTCAA AAATGTCATT TGGGTTTTAG ATTTTTCACA TACAATGATC	1320
AATTTTTC	1329

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1113 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..1113
 (D) OTHER INFORMATION: /note= "RAP2.8"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CGCCACCACC GCCAAGAAGC TCTCTCCTCC TCCCGCGGCG GCGTTACGCC TCTACCGGAT	60
GGGAAGCGGC GGGAGCAGCG TCGTGTTGGA TCCCGAGAAC GGCCTAGAGA CGGAGTCACG	120
AAAGCTACCA TCTTCAAAAT ACAAAGGTGT TGTTCCTCAG CCTAACGGAA GATGGGGAGC	180
TCAGATCTAC GAGAAGCACC AACGAGTATG GCTCGGGACT TTCAACGAGC AAGAAGAAGC	240
TGCTCGTTCC TACGACATCG CAGCTTGTAG ATTCCGTGGC CGCGACGCCG TCGTCAACTT	300
CAAGAACGTT CTGGAAGACG GCGATTTAGC TTTTCTTGAA GCTCACTCAA AGGCCGAGAT	360
CGTCGACATG TTGAGAAAAC AACTTACGC CGACGAGCTT GAACAGAACA ATAAACGGCA	420

GTTGTTTCTC TCCGTCGACG CTAACGGAAA ACGTAACGGA TCGAGTACTA CTCAAAACGA	480
CAAAGTTTTTA AAGACGTGTG AAGTTCTTTT CGAGAAGGCT GTTACACCTA GCGACGTTGG	540
GAAGCTAAAC CGTCTCGTGA TACCTAAACA ACACGCCGAG AAACACTTTC CGTTACCGTC	600
ACCGTCACCG GCAGTGAATA AAGGAGTTTT GATCAACTTC GAAGACGTTA ACGGTAAAGT	660
GTGGAGGTTT CGTTACTCAT ACTGGAACAG TAGTCAAAGT TACGTGTTGA CCAAGGGATG	720
GAGTCGATTC GTCAAGGAGA AGAATCTTCG AGCCGGTGAT GTTGTTACTT TCGAGAGATC	780
GACCGGACTA GAGCGGCAGT TATATATTGA TTGGAAAGTT CGGTCTGGTC CGAGAGAAAA	840
CCCGGTTTCA GTGGTGGTTC GGCTTTTTCGG AGTTGATATC TTTAATGTGA CCACCGTGAA	900
GCCAAACGAC GTCGTGGCCG TTTGCGGTGG AAAGAGATCT CGAGATGTTG ATGATATGTT	960
TGCGTTACGG TGTTCCAAGA AGCAGGCGAT AATCAATGCT TTGTGACATA TTTCCTTTTC	1020
CGATTTTATG CTTTCGTTTT TTAATTTTTT TTTTGTCAA GTTGTGTAGG TTGTGATTCA	1080
TGCTAGGTTG TATTTAGGAA AAGAGATAAG ACC	1113

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..417
 (D) OTHER INFORMATION: /note= "RAP2.9"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CGATCACGGA TCTGGCTTGG TTCATACAAA ACCGCCGTTG CCGCGGCACG GGCCTACGAT	60
ACCGCTGTGT TTTACTTACG TGGTCCTTCG GCGAGACTCA ATTTCCCTGA AGAGGTCTTT	120
AAGGATGGAA ACGGCGGTGA AGGCTTAGGA GGAGATATGT CTCCGACGTT GATACGGAAG	180
AAGGCGGCTG AGGTGGGAGC TAGAGTCGAC GCAGAGTTGC GGTTAGAGAA TAGGATGGTT	240
GAGAACTTAG ACATGAATAA GTTGCCGGAG GCATATGGAT TGTAATTTAT AGTTTGGTAG	300
TTTATAGGTT GGAGATTGCC CGGAGACAGA GTCAAACAGA GGTTCCTCTGA CTCATATGAG	360
GCATAATATA GTTAATATAG TAATTTTTGT TTTGAGCATA GTAATTATGT CATAACC	417

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..814

C. J. (D) OTHER INFORMATION: /note= "RAP2.10"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

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ATTTTTTGAA ACTTCTTCTC TTTTGC GGTT TCGTGTCCA CTCCTCTCTT CTTGGCCCAC      60
GTGTTTCATCA ATCTCTCCCT CCGCATGTAA TCGCTTCGCC GTCAATATCA CATCTTTCTT      120
CTTCTTTTATC TTTAAAATCT CTTTAGATCG ATTCTTTTGT GGATTCTTGA AATCTCCGGA      180
GAAAACCACT ATGGAGACGG CGACTGAAGT GGCCACGGTG GTGTCAACTC CGGCGGTTAC      240
GGTTGCGGCG GTGGCGACGA GGAAGAGAGA TAAGCCGTAT AAAGGGATAA GGATGAGGAA      300
GTGGGGGAAG TGGGTGGCGG AGATAAGAGA GCCTAATAAA AGGTCAAGGA TCTGGCTTGG      360
CTCTTACTCT ACTCCTGAAG CGGCGGCGCG TGCTTACGAC ACGGCGGTGT TTTATCTCCG      420
AGGTCCTTCT GCTCGGCTTA ACTTCCCGGA GCTTTTAGCC GGAGTGACGG TGACGGGAGG      480
AGGCGGAGGA GGAGTGAACG GTGGTGGAGA TATGTCGGCG GCGTATATAA GGAGAAAAGC      540
GGCGGAGGTT GGAGCACAAG TGGATGCGTT AGAAGCGGCG GGGGCGGGAG GGAATCGTCA      600
TCATCATCAT CATCAACATC AACGTGGTAA TCATGATTAC GTAGATAATC ATAGTGATTA      660
TCGTATTAAT GATGATCTTA TGGAGTGTAG TAGTAAAGAA GGGTTTAAGA GGTGTAATGG      720
ATCGTTGGAA CGGGTTGATT TAAACAAATT ACCCGATCCG GAAACTTCAG ATGACGATTA      780
GGAAAGCAAA AAATAGAAAC AAAAAAAAAA AAAA                                     814

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(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 933 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..933
- (D) OTHER INFORMATION: /note= "RAP2.11"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

```

AAAAAATAT GGAACATCAA ACAACTCCAA AGCAGAAAAC TAAGGAGAAG AGCAAAGGCA      60
ACAAGACTAA GTTGTGGGA GTTAGGCAAA GGCCTTCAGG AAAATGGGTG GCAGAGATCA      120
AAGACACTAC ACAAAGATA CGGATGTGGC TCGGAACCTT TGAAACCGCA GAAGAAGCCG      180
CTCGAGCCTA CGATGAAGCT GCATGTCTCT TACGTGGCTC CAATACTCGC ACCAATTTCTG      240
CAAACCATTT TCCTAACAAC TCACAACTAT CTTTGAAGAT CAGAAATCTT CTTCAACCAGA      300
AGCAGAGCAT GAAGCAGCAG CAACAACAAC AACACAAACC AGTTTCTTCT TTAACGGATT      360
GCAACATCAA CTACATCTCG ACTGCTACTA GTCTCACCAC AACCACCACC ACCACCACTA      420
CCACGGCCAT ACCGCTCAAT AATGTGTACC GACCAGATTC ATCGGTCATT GGGCAACCAG      480
AAACCGAGGG TCTCCAGCTT CTTATTCTGT GGCCCTTGT CTCTGGATTC AACCATCAGA      540
TTCCATTGGC TCAGGCAGGG GGAGAAACAC ATGGACATCT CAACGATCAC TACTCAACCG      600
ATCAACATTT GGGTCTTGCA GAAATTGAAA GACAGATATC TGCCTCCCTA TATGCAATGA      660
ATGGAGCTAA CAGTTACTAT GACAACATGA ATGCAGAATA TGCAATTTTC GATCCTACCG      720
ATCCCATTG GATCTCCCT TCACTCTCCC AACTCTTCTG CCCTACGTGA TTTCCAATTT      780
ACTTTTCCTG ATCAATTCAT GTAATGTTTG GATCAATGAT CCATGATTGT AAAGTAGAAC      840
ACATCTCTAC AATGTTCCAA TAGACAAGAT TGTACCTAAA GAAAATGGAC AATGTAAGAA      900
GATAATGAAG GTTTCGTACA ACAAAGCTT GAT                                     933

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(2) INFORMATION FOR SEQ ID NO:111:

CIA
WA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1277
- (D) OTHER INFORMATION: /note= "RAP2.12"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

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CGTTCGAATT TCTTCGATTT TGACGCTGAG TTCGAAGCTG ATTTCCAAGG TTTCAAAGAT      60

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GATTCGTCTA	TCGATTGCGA	TGATGATTTT	GACGTCGGTG	ATGTTTTTCGC	CGATGTGAAA	120
CCATTCGTTT	TCACTTCGAC	TCCAAAACCC	GCCGTCTCCG	CCGCTGCGGA	AGGTTTCAGTT	180
TTTGGTAAGA	AAGTTACTGG	CTTGGATGGG	GACGCTGAGA	AATCTGCAAA	TAGGAAGAGG	240
AAGAATCAGT	ACCGAGGGAT	TAGGCAACGT	CCTTGGGGAA	AATGGGCTGC	TGAGATACGT	300
GATCCAAGGG	AAGGTGCTAG	AATCTGGCTT	GGAACGTTCA	AGACAGCTGA	GGAAGCTGCT	360
AGAGCTTACG	ATGCTGCAGC	GCGGAGAATC	CGTGGATCTA	AAGCTAAGGT	GAATTTCCCT	420
GAAGAAAACA	TGAAGGCTAA	TTCTCAGAAA	CGCTCTGTGA	AGGCTAATCT	TCAGAAACCA	480
GTGGCTAAAC	CTAACCCTAA	CCCAAGTCCA	GCTTTGGTTC	AGAACTCGAA	CATCTCCTTT	540
GAAAATATGT	GTTTCATGGA	GGAGAAACAC	CAAGTGAGCA	ACAACAACAA	CAACCAGTTT	600
GGGATGACAA	ACTCCGTTGA	TGCTGGATGT	AATGGGTATC	AGTATTTTCAG	CTCTGACCAG	660
GGTAGTAATT	CTTTCGATTG	TTCGGAGTTT	GGTTGGAGCG	ATCAAGCTCC	GATAACTCCC	720
GACATCTCTT	CTGCGGTTAT	CAACAACAAC	AACTCAGCTC	TGTTCTTTGA	GGAAGCCAAT	780
CCAGCTAAGA	AGCTCAAGTC	TATGGATTTT	GAGACACCTT	ACAACAACAC	TGAATGGGAC	840
GCTTCACTGG	ATTTCTCTCA	CGAAGATGCT	GTAACGACTC	AGGACAATGG	TGCAAACCCT	900
ATGGACCTAT	GGAGTATTGA	TGAAATTCAT	TCCATGATTG	GAGGAGTCTT	CTGAAGAGAT	960
CCAGTTTCAT	GTAAATAAGG	CTGCATGTTT	GTGAGTTTCC	CGCATCGTTC	GTTTATCAAC	1020
CTCCAAAAC	TTCTAATGTC	TGTTACTTGC	ATCTTCTTCT	GCTGTCTCTG	TCTGTCTCTC	1080
TCAGGAGTTC	CTGTTTGCAT	TGCGAGAAGC	CATGAGCCTC	TATCTTGAGG	GTAGTTGTGA	1140
TGAAGTTAAG	TAGAGGCTTA	TTTTTAGGGG	TTGTGGTAGT	TTTTGTTTTA	GTGAATCTTT	1200
TGAATTCGTT	TGTGTTTTGT	TTTTGTACT	TTATGCCCCA	AAACTCCTTT	AACATTTGTC	1260
ATAATGTGTT	TGAACCT					1277

C1
6A